

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/510,413
Source: PCT
Date Processed by STIC: 07-05-2005

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PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/510,413

DATE: 07/05/2005
TIME: 11:06:25

Input Set : A:\8016-4-32448.corr-25-Nov-2003.ST25.txt
Output Set: N:\CRF4\07052005\J510413.raw

3 <110> APPLICANT: Novartis AG
 5 <120> TITLE OF INVENTION: Compound Screening
 7 <130> FILE REFERENCE: 4-32448A/NFI 8016
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/510,413
C--> 9 <141> CURRENT FILING DATE: 2004-10-06
 9 <160> NUMBER OF SEQ ID NOS: 16
 11 <170> SOFTWARE: PatentIn version 3.1
 13 <210> SEQ ID NO: 1
 14 <211> LENGTH: 326
 15 <212> TYPE: PRT
 16 <213> ORGANISM: human full-length sHuR
 18 <220> FEATURE:
W--> 19 <221> NAME/KEY: full-length sHuR human
 20 <222> LOCATION: (1)..(326)
 21 <223> OTHER INFORMATION:
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 25 Met Ser Asn Gly Tyr Glu Asp His Met Ala Glu Asp Cys Arg Gly Asp
 26 1 5 10 15
 29 Ile Gly Arg Thr Asn Leu Ile Val Asn Tyr Leu Pro Gln Asn Met Thr
 30 20 25 30
 33 Gln Asp Glu Leu Arg Ser Leu Phe Ser Ser Ile Gly Glu Val Glu Ser
 34 35 40 45
 37 Ala Lys Leu Ile Arg Asp Lys Val Ala Gly His Ser Leu Gly Tyr Gly
 38 50 55 60
 41 Phe Val Asn Tyr Val Thr Ala Lys Asp Ala Glu Arg Ala Ile Asn Thr
 42 65 70 75 80
 45 Leu Asn Gly Leu Arg Leu Gln Ser Lys Thr Ile Lys Val Ser Tyr Ala
 46 85 90 95
 49 Arg Pro Ser Ser Glu Val Ile Lys Asp Ala Asn Leu Tyr Ile Ser Gly
 50 100 105 110
 53 Leu Pro Arg Thr Met Thr Gln Lys Asp Val Glu Asp Met Phe Ser Arg
 54 115 120 125
 57 Phe Gly Arg Ile Ile Asn Ser Arg Val Leu Val Asp Gln Thr Thr Gly
 58 130 135 140
 61 Leu Ser Arg Gly Val Ala Phe Ile Arg Phe Asp Lys Arg Ser Glu Ala
 62 145 150 155 160
 65 Glu Glu Ala Ile Thr Ser Phe Asn Gly His Lys Pro Pro Gly Ser Ser
 66 165 170 175
 69 Glu Pro Ile Ala Val Lys Phe Ala Ala Asn Pro Asn Gln Asn Lys Asn
 70 180 185 190
 73 Val Ala Leu Leu Ser Gln Leu Tyr His Ser Pro Ala Arg Arg Phe Gly
 74 195 200 205
 77 Gly Pro Val His His Gln Ala Gln Arg Phe Arg Phe Ser Pro Met Gly

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78      210          215          220
81 Val Asp His Met Ser Gly Leu Ser Gly Val Asn Val Pro Gly Asn Ala
82 225          230          235          240
85 Ser Ser Gly Trp Cys Ile Phe Ile Tyr Asn Leu Gly Gln Asp Ala Asp
86          245          250          255
89 Glu Gly Ile Leu Trp Gln Met Phe Gly Pro Phe Gly Ala Val Thr Asn
90          260          265          270
93 Val Lys Val Ile Arg Asp Phe Asn Thr Asn Lys Cys Lys Gly Phe Gly
94          275          280          285
97 Phe Val Thr Met Thr Asn Tyr Glu Glu Ala Ala Met Ala Ile Ala Ser
98          290          295          300
101 Leu Asn Gly Tyr Arg Leu Gly Asp Lys Ile Leu Gln Val Ser Phe Lys
102 305          310          315          320
105 Thr Asn Lys Ser His Glu
106          325
109 <210> SEQ ID NO: 2
110 <211> LENGTH: 325
111 <212> TYPE: PRT
112 <213> ORGANISM: Homo sapiens
114 <220> FEATURE:
W--> 115 <221> NAME/KEY: sHuR
116 <222> LOCATION: (2)..(325)
117 <223> OTHER INFORMATION:
W--> 119 <400> 2
121 Ser Asn Gly Tyr Glu Asp His Met Ala Glu Asp Cys Arg Gly Asp Ile
122 1          5          10          15
125 Gly Arg Thr Asn Leu Ile Val Asn Tyr Leu Pro Gln Asn Met Thr Gln
126          20          25          30
129 Asp Glu Leu Arg Ser Leu Phe Ser Ser Ile Gly Glu Val Glu Ser Ala
130          35          40          45
133 Lys Leu Ile Arg Asp Lys Val Ala Gly His Ser Leu Gly Tyr Gly Phe
134          50          55          60
137 Val Asn Tyr Val Thr Ala Lys Asp Ala Glu Arg Ala Ile Asn Thr Leu
138 65          70          75          80
141 Asn Gly Leu Arg Leu Gln Ser Lys Thr Ile Lys Val Ser Tyr Ala Arg
142          85          90          95
145 Pro Ser Ser Glu Val Ile Lys Asp Ala Asn Leu Tyr Ile Ser Gly Leu
146          100         105         110
149 Pro Arg Thr Met Thr Gln Lys Asp Val Glu Asp Met Phe Ser Arg Phe
150          115         120         125
153 Gly Arg Ile Ile Asn Ser Arg Val Leu Val Asp Gln Thr Thr Gly Leu
154          130         135         140
157 Ser Arg Gly Val Ala Phe Ile Arg Phe Asp Lys Arg Ser Glu Ala Glu
158 145          150          155          160
161 Glu Ala Ile Thr Ser Phe Asn Gly His Lys Pro Pro Gly Ser Ser Glu
162          165          170          175
165 Pro Ile Ala Val Lys Phe Ala Ala Asn Pro Asn Gln Asn Lys Asn Val
166          180          185          190
169 Ala Leu Leu Ser Gln Leu Tyr His Ser Pro Ala Arg Arg Phe Gly Gly

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170	195	200	205
173	Pro Val His His Gln Ala Gln Arg Phe Arg Phe Ser Pro Met Gly Val		
174	210	215	220
177	Asp His Met Ser Gly Leu Ser Gly Val Asn Val Pro Gly Asn Ala Ser		
178	225	230	235
181	Ser Gly Trp Cys Ile Phe Ile Tyr Asn Leu Gly Gln Asp Ala Asp Glu		240
182	245	250	255
185	Gly Ile Leu Trp Gln Met Phe Gly Pro Phe Gly Ala Val Thr Asn Val		
186	260	265	270
189	Lys Val Ile Arg Asp Phe Asn Thr Asn Lys Cys Lys Gly Phe Gly Phe		
190	275	280	285
193	Val Thr Met Thr Asn Tyr Glu Glu Ala Ala Met Ala Ile Ala Ser Leu		
194	290	295	300
197	Asn Gly Tyr Arg Leu Gly Asp Lys Ile Leu Gln Val Ser Phe Lys Thr		
198	305	310	315
201	Asn Lys Ser His Glu		320
202	325		
205	<210> SEQ ID NO: 3		
206	<211> LENGTH: 189		
207	<212> TYPE: PRT		
208	<213> ORGANISM: Homo sapiens		
210	<220> FEATURE:		
W-->	211 <221> NAME/KEY: HuR12		
212	<222> LOCATION: (1)..(189)		
213	<223> OTHER INFORMATION:		
W-->	215 <400> 3		
217	Met Ser Asn Gly Tyr Glu Asp His Met Ala Glu Asp Cys Arg Gly Asp		
218	1	5	10
221	Ile Gly Arg Thr Asn Leu Ile Val Asn Tyr Leu Pro Gln Asn Met Thr		15
222	20	25	30
225	Gln Asp Glu Leu Arg Ser Leu Phe Ser Ser Ile Gly Glu Val Glu Ser		
226	35	40	45
229	Ala Lys Leu Ile Arg Asp Lys Val Ala Gly His Ser Leu Gly Tyr Gly		
230	50	55	60
233	Phe Val Asn Tyr Val Thr Ala Lys Asp Ala Glu Arg Ala Ile Asn Thr		
234	65	70	75
237	80		
238	Leu Asn Gly Leu Arg Leu Gln Ser Lys Thr Ile Lys Val Ser Tyr Ala		
241	85	90	95
242	Arg Pro Ser Ser Glu Val Ile Lys Asp Ala Asn Leu Tyr Ile Ser Gly		
245	100	105	110
246	Leu Pro Arg Thr Met Thr Gln Lys Asp Val Glu Asp Met Phe Ser Arg		
249	115	120	125
250	Phe Gly Arg Ile Ile Asn Ser Arg Val Leu Val Asp Gln Thr Thr Gly		
253	130	135	140
254	Leu Ser Arg Gly Val Ala Phe Ile Arg Phe Asp Lys Arg Ser Glu Ala		
257	145	150	155
258	Glu Glu Ala Ile Thr Ser Phe Asn Gly His Lys Pro Pro Gly Ser Ser		160
261	165	170	175
	Glu Pro Ile Ala Val Lys Phe Ala Ala Asn Pro Asn Gln		

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Input Set : A:\8016-4-32448.corr-25-Nov-2003.ST25.txt
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262 180 185
 265 <210> SEQ ID NO: 4
 266 <211> LENGTH: 188
 267 <212> TYPE: PRT
 268 <213> ORGANISM: Homo sapiens
 270 <220> FEATURE:
 W--> 271 <221> NAME/KEY: HuR12
 272 <222> LOCATION: (2)..(188)
 273 <223> OTHER INFORMATION:
 W--> 275 <400> 4
 277 Ser Asn Gly Tyr Glu Asp His Met Ala Glu Asp Cys Arg Gly Asp Ile
 278 1 5 10 15
 281 Gly Arg Thr Asn Leu Ile Val Asn Tyr Leu Pro Gln Asn Met Thr Gln
 282 20 25 30
 285 Asp Glu Leu Arg Ser Leu Phe Ser Ser Ile Gly Glu Val Glu Ser Ala
 286 35 40 45
 289 Lys Leu Ile Arg Asp Lys Val Ala Gly His Ser Leu Gly Tyr Gly Phe
 290 50 55 60
 293 Val Asn Tyr Val Thr Ala Lys Asp Ala Glu Arg Ala Ile Asn Thr Leu
 294 65 70 75 80
 297 Asn Gly Leu Arg Leu Gln Ser Lys Thr Ile Lys Val Ser Tyr Ala Arg
 298 85 90 95
 301 Pro Ser Ser Glu Val Ile Lys Asp Ala Asn Leu Tyr Ile Ser Gly Leu
 302 100 105 110
 305 Pro Arg Thr Met Thr Gln Lys Asp Val Glu Asp Met Phe Ser Arg Phe
 306 115 120 125
 309 Gly Arg Ile Ile Asn Ser Arg Val Leu Val Asp Gln Thr Thr Gly Leu
 310 130 135 140
 313 Ser Arg Gly Val Ala Phe Ile Arg Phe Asp Lys Arg Ser Glu Ala Glu
 314 145 150 155 160
 317 Glu Ala Ile Thr Ser Phe Asn Gly His Lys Pro Pro Gly Ser Ser Glu
 318 165 170 175
 321 Pro Ile Ala Val Lys Phe Ala Ala Asn Pro Asn Gln
 322 180 185
 325 <210> SEQ ID NO: 5
 326 <211> LENGTH: 34
 327 <212> TYPE: RNA
 328 <213> ORGANISM: Homo sapiens
 330 <220> FEATURE:
 W--> 331 <221> NAME/KEY: ARE sequence of human TNF-alpha
 332 <222> LOCATION: (1)..(34)
 333 <223> OTHER INFORMATION:
 W--> 335 <400> 5
 336 auuauuuauu auuuauuuau uauuuauuuua uuuua 34
 339 <210> SEQ ID NO: 6
 340 <211> LENGTH: 33
 341 <212> TYPE: RNA
 342 <213> ORGANISM: Homo sapiens
 344 <220> FEATURE:

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Input Set : A:\8016-4-32448.corr-25-Nov-2003.ST25.txt
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W--> 345 <221> NAME/KEY: ARE sequence of human IL-2

346 <222> LOCATION: (1)..(33)

347 <223> OTHER INFORMATION:

W--> 349 <400> 6

350 uauuuuauua aauauuuaaa uuuuauauuu auu

33

353 <210> SEQ ID NO: 7

354 <211> LENGTH: 33

355 <212> TYPE: RNA

356 <213> ORGANISM: Homo sapiens

358 <220> FEATURE:

W--> 359 <221> NAME/KEY: ARE sequence of IL-1 beta

360 <222> LOCATION: (1)..(33)

361 <223> OTHER INFORMATION:

W--> 363 <400> 7

364 uauuuuauua uuuauuuugu uguuuguuuu auu

33

367 <210> SEQ ID NO: 8

368 <211> LENGTH: 56

369 <212> TYPE: RNA

370 <213> ORGANISM: Homo sapiens

372 <220> FEATURE:

W--> 373 <221> NAME/KEY: ARE sequence of human IL-4

374 <222> LOCATION: (1)..(56)

375 <223> OTHER INFORMATION:

W--> 377 <400> 8

378 auuuuaauuu augaguuuuu gauagcuuuua uuuuuuaagu auuuauauau uuauaa

56

381 <210> SEQ ID NO: 9

382 <211> LENGTH: 26

383 <212> TYPE: RNA

384 <213> ORGANISM: Homo sapiens

386 <220> FEATURE:

W--> 387 <221> NAME/KEY: ARE sequence of human IL-8

388 <222> LOCATION: (1)..(26)

389 <223> OTHER INFORMATION:

W--> 391 <400> 9

392 uauuuuauua uaauguauuu auuuuaa

26

395 <210> SEQ ID NO: 10

396 <211> LENGTH: 35

397 <212> TYPE: RNA

398 <213> ORGANISM: Homo sapiens

400 <220> FEATURE:

W--> 401 <221> NAME/KEY: ARE sequence of human Cox-2

402 <222> LOCATION: (1)..(35)

403 <223> OTHER INFORMATION:

W--> 405 <400> 10

406 uauuaauuuua auuaauuuuaau aauauuuuaau uaaaaa

35

409 <210> SEQ ID NO: 11

410 <211> LENGTH: 17

411 <212> TYPE: RNA

412 <213> ORGANISM: artificial

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 07/05/2005
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Input Set : A:\8016-4-32448.corr-25-Nov-2003.ST25.txt
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:11,12,13,14,15,16

VERIFICATION SUMMARY DATE: 07/05/2005
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Input Set : A:\8016-4-32448.corr-25-Nov-2003.ST25.txt
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L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:19 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:23 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:21
L:115 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:119 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:117
L:211 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:215 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:213
L:271 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:275 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:273
L:331 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:335 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:333
L:345 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:349 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:347
L:359 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:363 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:361
L:373 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:377 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:375
L:387 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
L:391 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:389
L:401 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:405 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10,Line#:403